Table 1

EAA (essential amino ad	ids)	NEAA (non-essential a acids)	aino
L-arginine HCl	126.4 mg/l	L-alanine	8.9 mg/l
L-cystine	24.02 mg/l	L-asparagine	13.2 mg/l
L-histidine HCI H2O	41.92 mg/l	L-aspartic-acid	13.3 mg/l
L-isoleucine		L-glutamic acid	14.7 mg/l
L-leucine	52.46 mg/l	glycine	7.5 mg/l
L-lysine HCl	73.06 mg/l	L-prolin	11.5 mg/l
L-methionine	14.92 mg/l	L-serine	10.5 mg/l
L-phenylalanine	33.02 mg/l		
L-threonine	47.64 mg/l		
L-tryptophane	10.2 mg/l		
L-tyrosine	36.22 mg/l		
L-valine	46.86 mg/l		

Single amino acide	5
histidine HCI H2O	20 mg/l
isoleucine	50 mg/l
leucine	50 mg/l
methionine	15 mg/l
phenylalanine	15 mg/l
threonine	20 mg/l
tyrosine	20 mg/l
arginine HCI	240 mg/l
lysine	40 mg/l
D-lysine	40 mg/l
cystine	50 mg/l
tryptophane	5 mg/l
valine	20 mg/l
glutamine	300 mg/l



Table 2. APIT kills different tumor cell lines

models for	kind of tumor	tumor cell line IC	IC50 (ng/ml)
1. solid tumors	lung cancer breast cancer prostate cancer colon cancer cervix cancer uterus carcinoma larynx cancer stomach cancer	GLC4 MCF-7, SK-BR-3 PC3, DU145 HT-29 HeLa, Chang Hec-1-B AGS Hep-2 AGS	20 * * * * *
2. leukemia	T cell leukemia (ALL) T cell leukemia (ALL) B cell leukemia Monocyte leukemia (AML) Monocyte leukemia (AML)	Jurkat neo CEM neo SKW neo Mono Mac 6 THP-1	3.2 3.6 * 10
3. "orphan" tumors	Ewings sarcoma	RDES A673	4.5
4. apoptosis resistant tumors	(CML) T cell leukemia (ALL) T cell leukemia (ALL) B cell leukemia	K562 Jurkat BcI-2 CEM BcI-X _L SKW BcI-2	4.25 2.7 4.0 5.5
5. MDR tumors	Lung cancer	GLC4-ADR	10

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Description	gi	NCBI	NCBI version	swissprot	effect
F C.4.1.2.13)	229674	1ALD	1ALD	P04075	٠
rv chain 12	2134660	S65491	S65491	1	•
	2078327	AAB54008	AAB54008.1	Q16836	
plasmic (C1-THF synthase)	115206	P11586	P11586	P11586	•
Form	20151189	1L1F_A	1L1F_A	-	E
	4885281	NP_005262	NP_005262.1	P00367	
Cleavage and nolyadenylation specific factor 5, 25 kD subunit	5901926	NP_008937	NP_008937.1		+
1	5031635	NP_005498	NP_005498.1	P23528	ı
Coronin, actin binding protein, 1A	5902134	NP_009005	NP_009005.1	P31146	+
Dihydrolipoamide dehydrogenase precursor; E3 component of pyruvate	4557525 .	00000 AN	NP_000099.1	P09622	•
dehydrogenase	12314022	CAC14088	CAC14088.1		+
UNA replication licensing factor MCM4	1705520			P33991	+
Floroation factor 1-delta (EF-1-delta)	20141357	P29692 .	P29692	P29692	
Fnolase 1 alpha: phosphopyruvate hydratase	4503571	NP 001419	NP_001419.1	Q05524	+
	31645	CAA25833	CAA25833.1	P04406*	+
	35053	CAA37794	CAA37794.1	P04406*	
Heat shock 60kD protein 1 (chaperonin)	14603309	AAH10112	AAH10112.1	Q96FZ6	•
Heat shock 60kDa protein 1 (chaperonin)	4504521	NP 002147	NP_002147.1	P10809	_
Heat shock 70kD protein 9B (mortalin-2)	4758570	NP_004125	NP_004125.1	Q8N1C8	'
in C, Isoform b	4758544	NP_004491	NP_004491.1	P07910	E
	6841456	AAF29081	AAF29081.1	Q9P037	Ε
Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2)	124419	P12268	P12268	P12268	+
Isocitrate dehydrogenase 3 (NAD+) alpha	5031777	NP_005521	NP 005521.1	P50213	"
KH-type splicing regulatory protein (FUSE binding protein 2)	4504865	NP_003676	NP_003676.1	,	•
Nuclear matrix protein NMP200 related to splicing factor PRP19	7657381	NP_055317	NP 055317.1	Q9UMS4	•
Nucleobindin 2	4826870	NP_005004	NP_005004.1	P80303	1
54 kDa nuclear RNA- and DNA-binding protein (p54(nrb)) (p54nrb)	13124797	Q15233	Q15233	Q15233	+
Peroxiredoxin 1 (Thioredoxin peroxidase 2)	548453	Q06830	Q06830	Q06830	Ε
Peroxiredoxin 1; Proliferation-associated gene A; proliferation-associated	4505591	NP_002565.1	NP_002565.1	Q06830	E

Table 3. Continuation I

		NODI	NOBL vorcion	1 +0.0000	100
Description	Ŋ.	IACDI	NCDI VELSIOII	รพเธรุมเดเ	ellect
Peroxiredoxin 2 (Thioredoxin peroxidase 1)	2507169	P32119	P32119	P32119	+
Peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide	5802974	NP_006784	NP_006784.1	P30048	,
reductase precursor					
2-phosphopyruvate-hydratase alpha-enolase; carbonate dehydratase	693933	CAA59331	CAA59331.1	P06733	+
Proteasome subunit alpha type 7	12643540	014818	014818	014818	+
Proteasome subunit beta type 1 (Proteasome component C5) (Macropain	130853	P20618	P20618	P20618	+
		·			
Ras-GTPase-activating protein SH3-domain-binding protein; GAP binding	5031703	NP_005745.1	NP_005745.1	Q13283	E
protein	-				
Replication protein A2, 32kDa	4506585	NP_002937	NP_002937.1	P15927	
Rho GDP-dissociation Inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)	1707893	P52566	P52566	P52566	
Ribosomal protein P0; 60S acidic ribosomal protein P0	4506667	NP_000993	NP_000993.1	P05388	,
or similar BLOCK 23	20536934	XP_165448	XP_165448.1	Q8NHW5	
Ribosomal protein, large, P0	12654583	AAH01127	AAH01127.1	P05388	,
RNA-binding protein regulatory subunit	6005749	NP_009193	NP_009193.1	014805	+
RNA-binding protein regulatory subunit	12720028	XP_001707	XP_001707.2	014805	+
Semenogelin I; Semenogelin	4506883	NP_002998	NP_002998.1	P04279	
Similar to villin 2 (ezrin)	15530243	AAH13903 .	AAH13903.1	P15311	,
Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	4826998	NP_005057	NP_005057.1	P23246	1
Stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19;	5031851	NP_005554	NP_005554.1		1.
leukemla-associated phosphoprotein p18					
U2 small nuclear ribonucleoprotein A' (U2 snRNP-A')	134094	P09661	P09661	P09661	+
Vimentin	4507895	NP_003371	NP_003371.1	P08670	
Voltage-dependent anion-se ective channel protein 2 (VDAC-2) (hVDAC2)	1172554	P45880	P45880	P45880	

Table 4. Transcriptome analysis

Unigene cluster Description	Description	GENE	į	pir/NCBI/ewieen offect	offort
Hs.3833	3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1	85537	NID OOE434 4	50
LL 166563		100 10 1	100000	1000404.1	
118.100303	I Epilicalion Lacio Color (acuvator 1) 1, 140KDa	자-C1	15011931	15011931 ref:NP 002904.2	1
Hs.78991	DNA segment, numerous copies, expressed probes (GS1 gene).	DXF68S1E		ref:NP_036212.1	•
Hs.326035	early growth response 1	EGR1	119242	sp:P18146	‡
Hs.108885	collagen, type VI, alpha 1	COL6A1	15011913	15011913 ref:NP 001839.1	++
Hs.78944	regulator of G-protein signalling 2, 24kDa	RGS2	2135146	pir:153020	‡
Hs.110571	growth arrest and DNA-damage-inducible, beta	GADD45B	9945332	ref:NP 056490.1	‡
Hs.78465	v-jun sarcoma virus 17 oncogene homolog (avian)	, NOC	135298	sp:P05412	+
Hs.82646	DnaJ (Hsp40) homolog, subfmaily B; member 1	DNAJB1	1706473	sp:P25685	+
Hs.169840	TTK protein kinase	TTK	346403	pir:A42861	+
Hs.211601	mitogen-activated protein kinase kinase klase 12	MAP3K12	18202489 sp:Q12852	sp:Q12852	+
Hs.345728	suppressor of cytokine signaling 3	SSI-3	4507235	ref:NP_003946.1	+
Hs.3776	zinc finger protein 216	ZNF216	5174755	ref:NP 005998.1	+
Hs.73037		CNR2	450068	prf:1920360A	+
Hs.167578	EST, FLJ25357 hypothetical protein FLJ25357		740170	2004399A	+
Hs.8715	hypothetical protein MGC3232	MGC3232	3024681	sp:000268	+
Hs.74520	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	SCA1	1082237	pir:S46268	+
Hs.6151	pumilio homolog 2 (Drosophila)	PUM2	14277945 pdb:11B3	odb:11B3	+
Hs.8026	EST, Highly similar to SES2_HUMAN Sestrin 2 [H.sapiens]		13633882 sp:P58004	sp:P58004	+
Hs.82173	TGFB inducible early growth response	TIEG	11387050 sp:Q13118	sp:Q13118	+
Hs.198307	von Hippel-Lindau binding protein 1	VBP1	4507873 r	4507873 ref:NP 003363.1	+
Hs.179982	tumor protein p53-binding protein	TP53BPL	5032191	ref:NP_005793.1	+
Hs.2549	adrenergic, beta-3-, receptor	ADRB3	1070630	pir:QRHUBE	+
Hs.2128	dual specificity phosphatase 5	DUSP5	12707566	12707566 ref:NP_004410.2	+
Hs.36927	heat shock 105kD	HSP105B	5729879 r	ref:NP 006635.1	+
Hs.77558	high mobility group nucleosomal binding domain 3	HMGN3	4	sp:Q15651	+
Hs.460	activating transcription factor 3	ATF3	88875 p	pir:C34223	+
Hs.104125	adenylyl cyclase-associated protein	CAP	399184 s	sp:Q01518	+
Hs.24719	modulator of apoptosis 1	MAP-1	11545896 r	11545896 ref:NP 071434.1	+
Hs.8257	cytokine Inducible SH2-containing protein	CISH	13124022 sp:Q9NSE2	p:Q9NSE2	<u>,</u> +
Hs.101383	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments)		2135765 pir:A43932	ir:A43932 ·	+

Table 4. Continuation l

able 4. Continuation	วที่เกินสเจน เ				
Unigene cluster	Description	GENE	_	pir/NCBI/swisspr	effect
Hs 276770	CDW52 antiden (CAMPATH-1 antigen)	CDW52	4502761	ref:NP_001794.1	+
He BOB4	hypothetical protein dJ465N24.2.1	DJ465N24.2.1	10092679	DJ465N24.2.1 10092679 ref:NP_064713.1	+
He 78879	Thinnilin specific protease 10	USP10	11360280	11360280 pir: T47164	+
He 880	Charot-I evden crystal protein	CLC	1942631	pdb:1LCL	+
He 277401	Ihromodomain adjacent to zinc finger domain, 2A	BAZ2A	7304921	ref:NP_038477.1	+
He 300863	Jiethal (3) malignant brain tumor I(3)mbt protein (Drosophila) horrolog	H-L(3)MBT	14141728	14141728 ref:NP_056293.2	+
Hs 4557	Inbiguilln 2	UBQLN2	16753207	16753207 ref:NP_038472.2	+
Hs 151903	GroE-like protein cochaperone	HMGE	18202951	18202951 sp:Q9HAV7	+
He 36606	FST. Weakly similar to T29982 hypothetical protein F11G11.12 - [C. elegans]		_	٠	+
Hs 85302	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	ADARB1	2829669	sp:P78563	+
He 113823	ClnX caseinolytic protease X homolog (E. coli)	CLPX	14916956	14916956 sp:076031	+
He 25911	HLA-B associated transcript 2	BAT2	18375626	18375626 ref:NP_542417.1	+
He 05821	osteoclast stimulating factor 1	OSTF1	11134088	11134088 sp.Q92882	+
Hs 11217	KIAA0877 protein	KIAA0877			+
He 301064	arfactin 1	HSU52521	1703203	sp:P53367	+
HS:001001	FST Moderately similar to kinase suppressor of ras [Mus musculus]			-	+
He 211569		GPRK5	2135145	pir:A48277	+
Hs 25524	profein (vrosine phosphatase, non-receptor type 23	PTPN23	7512735	pir:T14756	+
He 94498	Heukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2	5803068	5803068 ref:NP_006857.1	+
Hs 24427	DKFZP56601646 protein	DC8	7512839	pir:T08737	+
Hs 46	platelet-activating factor receptor	PTAFR	107346	pir:A40191	+
Hs.90800	EST, Highly similar to matrix metalloproteinase 16, isoform 1; membrane-type matrix		13027802	13027802 ref:NP_005932.2	+
	metalloproteinase 3; membrane-type-3 matrix metalloproteinase [Homo sapiens]				
Hs.81648	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4	FLJ11021	2833266	sp:Q15696	+
Hs.80338	Bcl-2-associated transcription factor	ВТЕ	7661958	ref:NP_055554.1	+
Hs 238407	EST, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		8923452	ref:NP_060312.1	+
Hs 154668	KIAA039' gene product	KIAA0391	3024899	sp:O15091	+
Hs 76666	chromoscime 9 open reading frame 10	C9orf10	13431358	13431358 sp:Q9NZB2	+
Hs 9701	growth arrest and DNA-damage-inducible, gamma	GADD45G		ref:NP_006696.1	÷
Hs 100527	connector enhancer of KSR2	CNK2	7662368	ref:NP_055742.1	+
Hs 77274	plasminogen activator, uroklnase	PLAU	224665	prf:1110198A	+

Table 4. Continuation II

Unigene cluster Description		GENE	- 2	hir/NCD1/2	1
He 03516	10 T	i. 17	3	pillicoliswissi	enect
113.33310	L218				1
Hs.376709	Homo sapiens cDNA FLJ33768 fis, clone BRHIP2000021				- -
Hs.110299	milogen activated protein kinasa kinasa 7				+
		MAP2K/	4826946	4826946 ref:NP 005034.1	+
Hs.31396	ESTs, Weakly similar to S28807 collagen alpha 1(X) chain precursor IM.musculusi				
Hs.129715	gonadotropin-releasing hormone 2	CHOIL	2010725	111000	+
010007		211215	00/0160	3813733 Sp.: 043555	+
HS.1693/0	FYN oncogene related to SRC, FGR, YES	FYN	125370	125370 en.P06241	-
Hs.82007	methionyl aminopeptidase 1	METAP1	1703270	1703270 co.DE2E92	-
He 230018	DAB44B momber DAS and the first		1100510	Sp.r. 33302	
18.233010	INTERPORTED INTERP	RAB11B	1082426	1082426 hir IC2487	-
Hs.126852	solute carrier family 6 (neurotransmitter fransmorter GARA) member 13	C1 CE A 43	7707720	P. 10 22 TO	-
	of the state of th	0 FC0A10	85000//	1. 669/40 ANJEL 6560//	+

GENBANK		SYMBOL	EFFECT
	GENENAME		
NM 005252	v-fos FBJ murine osteosarcoma viral oncogene homolog		++
NM 006705	growth arrest and DNA-damage-inducible, gamma	45G	‡
NM_001964	early growth response 1	EGR1 *	‡
NM_002228	v-jun sarcoma virus 17 oncogene homolog (avian)	米 NDC	÷
NM_015675	growth arrest and DNA-damage-inducible, beta	GADD45B ¾	+
NM 001124	adrenomedullin	ADM	++
NM_005346	heat shock 70kDa protein 1B	HSPA1B	‡
NM 002166	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	1D2	‡
NM 004417	dual specificity phosphatase 1	DUSP1	‡
NM_003745	suppressor of cytokine signaling 1	SOCS1	‡
NM_002923	regulator of G-protein signalling 2, 24kDa	RGS2 *	‡
NM 005627	serum/glucocorticold regulated kinase	SGK	‡
BC012321	activity-regulated cytoskeleton-associated protein	ARC	‡
NM 025195	phosphoprotein regulated by mitogenic pathways	CBFW	+
NM 030751	transcription factor 8 (represses interleukin 2 expression)	TCF8	+
NM 014330	protein phosphatase 1, regulatory (inhibitor) subunit 15A	PPP1R15A	+
NM 004083	DNA-damage-inducible transcript 3	DDIT3	+
NM 001841	cannabinoid receptor 2 (macrophage)	K CNR2 ★	+
NM 004024	activating transcription factor 3	ATF3 米	+
NM 001706	B-cell CLL/lymphoma 6 (zinc finger protein 51)		+
NM 004428	ephrin-A1		+
NM_004419	dual specificity phosphatase 5	₩ 9dSna	+
NM_003088	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1	+
AB014566	dishevelled associated activator of morphogenesis 1		4
NM_006145	DnaJ (Hsp40) homolog, subfmally B, member 1	DNAJB1 米	+
NM_004962	growth differentiation factor 10.	GDF10	+
D79994	kidney ankyrin repeat-containing protein	İ	+
NM_006301	mitogen-activated protein kinase kinase kinase 12	MAP3K12 *	+
NM_002928	regulator of G-protein signalling 16	RGS16	+
NM 003955	suppressor of cytokine signaling 3	SOCS3	+
NM_004430	early growth response 3	EGR3	+
NM_001731	B-cell translocation gene 1, anti-proliferative	BTG1	+
NM_012342	putative transmembrane protein	NMA	+
NM_002262	killer cell lectin-like receptor subfamily D, member 1		+
NM_006007	zinc finger protein 216	ZNF216 来	+
NM_000905	neuropeptide Y	ΛPΥ	+

Table 5. (continued) 1	Table 5. (continued) Transcriptome analysis	IODVINO	EEEEOT
GENBANK		STINDOL	1011
NM 004418	dual specificity phosphatase 2	DUSPZ	+
NM 031459	sestrin 2	SES2	+
AF332558	BCL2 binding component 3	BBC3	+
NM 006000	tubulin, alpha 1 (testis specific)	TUBA1	+
NM 006644	heat shock 105kDa/110kDa protein 1	HSPH1	+
L24498	growth arrest and DNA-damage-inducible, alpha	GADD45A	+
AK024029	modulator of apoptosis 1	MOAP1	+
NM 005409	chemokine (C-X-C motif) ligand 11	CXCL11	+
NM 003383	very low density lipoprotein receptor	VLDLR	+
AF267856		DJ465N24.2.14	+
NM 002450	metallothionein 1L		+
NM 001828	Charot-Leyden crystal protein	∜ CLC	+
NM 013370	pregnancy-induced growth inhibitor	OKL38	÷
AB014581	I(3)mbt-like (Drosophila)	L3MBTL	+
NM 006875	pim-2 oncogene	PIM2	+
AL031665	actin, gamma pseudogene 3.	ACTGP3	+
Al985514		RPS19	+
NM 080686	HLA-B associated transcript 2	BAT2	+
NM 021184	chromosome 6 open reading frame 47	£47	+
NM 015471	DKFZP56601646 protein	₩ DC8	+
NM 000952	sceptor	PTAFR	+
BC012625	protein phosphatase 1, regulatory (inhibitor) subunit 3C		+
NM 023012	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4.	FLJ11021 米	+
AK024358	macrophage expressed gene 1	LOC219972	+
NM 002658	plasminogen activator, urokinase	PLAU *	÷
U12767	4, group A, member 3	NR4A3	+
NM 016615	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	SLC6A13	+
NM_002135	nuclear receptor subfamily 4, group A, member 1	NR4A1	+
AJ251595	CD44 antigen (homing function and Indian blood group system)	CD44	•
NM 005433	v-yes-1 Yamaquchi sarcoma viral oncogene homolog 1	YES1	,
NM 006325	RAN. member RAS oncogene family	RAN	١
NM 004775	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6	1
AK056671		UREB1	2
NM 022817	period homolog 2 (Drosophila)	PER2	•
L07044	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CAMK2G	1
NM 014890	downregulated in ovarian cancer 1	D0C1	1
			·

Table 5. (continued) Transcriptome analysis	anscrintome analysis		
GENBANK	GENENAME	SYMBOL	EFFECT
NM 001782	CD72 antiden	CD72 i	,
NM 005766	FERM. RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	FARP1 :	•
NM 000566	1::=	FCGR1A	-
NM 003036	v-ski sarcoma viral oncogene homolog (avlan)	SKI	-
NM 001713	betaine-homocysteine methyltransferase	BHMT ,	,
NM 001682	ATPase, Ca++ transporting, plasma membrane 1	ATP2B1	•
NM 003985	tyrosine kinase, non-receptor, 1	TNK1	
NM 004752	Idial cells missing homolog 2 (Drosophila)	GCM2	1
BC001619		ALDH1B1	1
NM 002422		MMP3	•
NM 003024		ITSN1	•
NM 002613	3-phosphoinositide dependent protein kinase-1	PDPK1	•
NM 000098	carnitine palmitoyltransferase II	CPT2	,
BC002712	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	MYCN	•
NM 003112	Sp4 transcription factor	SP4	-
NM 012062	dynamin 1-like	DNM1L	,
NM 000880	Interleukin 7	11.7	-
NM 004564	PET112-like (yeast)	PET112L	•
NM 001771	CD22 antigen	CD22	,
AA904067	protein phosphatase 1, regulatory (inhibitor) subunit 12B	PPP1R12B	-
NM 001633	alpha-1-microglobulin/bikunin precursor	AMBP	-
NM 007216	Hermansky-Pudlak syndrome 5	HPS5	-
AV708310	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	PPP2CA	•
AF296765	cerebral cavernous malformations 1	CCM1	1
AF155117	kinesin family member 21A	KIF21A	ı
NM 002006	pasic)	FGF2	•
NM 004362		CLGN	,
NM 021221	lymphocyte antigen 6 complex, locus G5B	LY6G5B	1
AK001541	secretory carrier membrane protein 1	SCAMP1	•
H08291	acid phosphatase 1, soluble	ACP1	
NM 014636	Ral guanine nucleotide exchange factor RaiGPS1A	RALGPS1A	•
NM 053006	serine/threonine kinase 22B (spermiogenesis associated)	STK22B	1
NM 000220	potassium inwardly-rectifying channel, subfamily J, member 1	KCNJ1	-
NM 000633	B-cell CLL/lymphoma 2	BCL2	,
100000	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-	OGT	
CUOSUU MINI	lacetylglucosaitiityt tratisterase/		

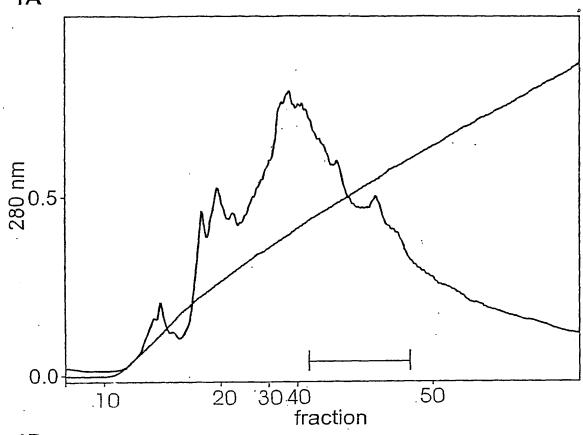
1,000,000

GENERAME TO millochondrial membrane 40 homolog (yeast) TO domain, EGF-like 2 MS se subtilish/kexin type 1 PS variant translocation 1 PS sarcoma viral oncogene homolog 1 AL sarcoma viral oncogene homolog 1 AL Si (HTFG) PD 3(HTFG) PD 3(HTFG) PD 3(HTFG) AL 4 AB AL 4 States and Ale AL 4 States and Ale AL 5 Telement binding protein 1 AL <t< th=""><th>Table 5. (continued) 7</th><th>Table 5. (continued) Transcriptome analysis</th><th></th><th>٠.</th></t<>	Table 5. (continued) 7	Table 5. (continued) Transcriptome analysis		٠.
Itensilocase of ouler milochondrial membrane 40 homolog (yeast) Inresolicase of ouler milochondrial membrane 40 homolog (yeast) Inresolication Inresolication Includer (yeast) I	GENBANK		SYMBOL	EFFECT
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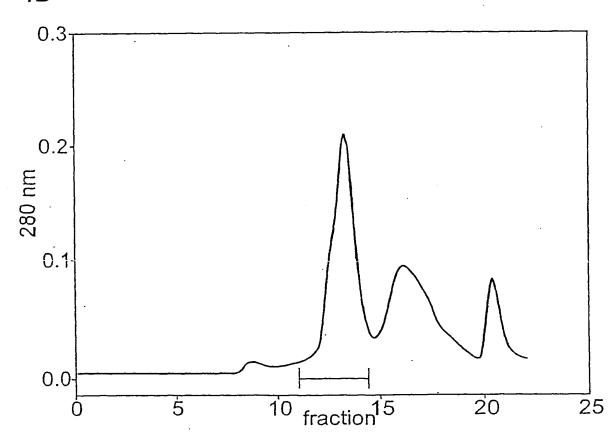
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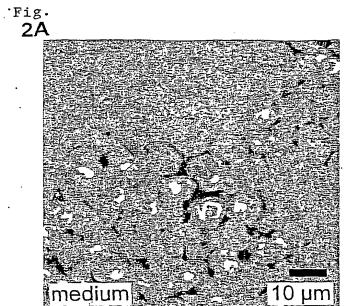


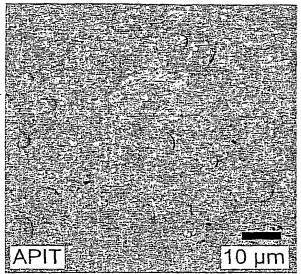
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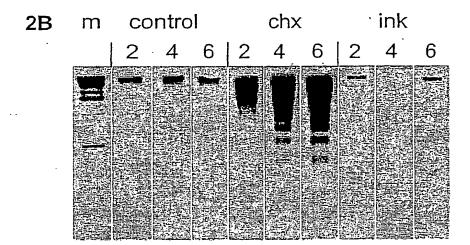
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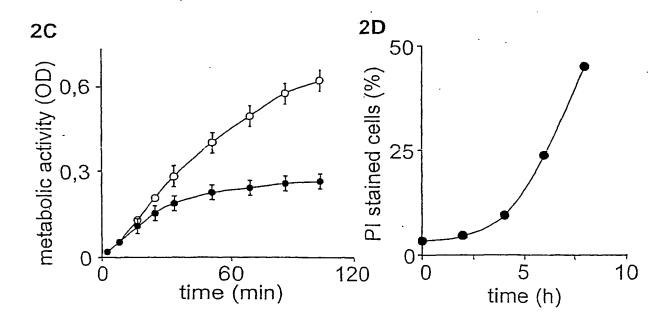


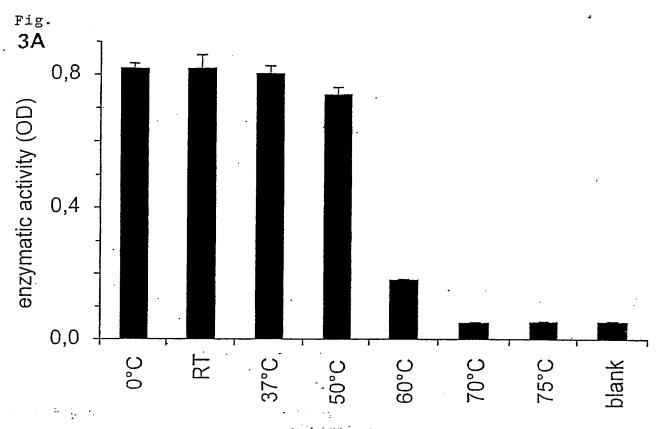


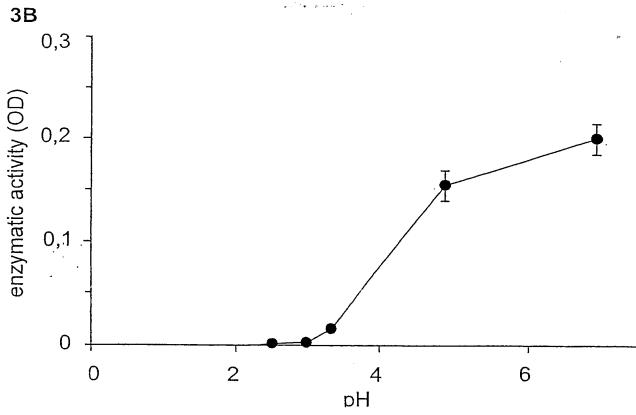


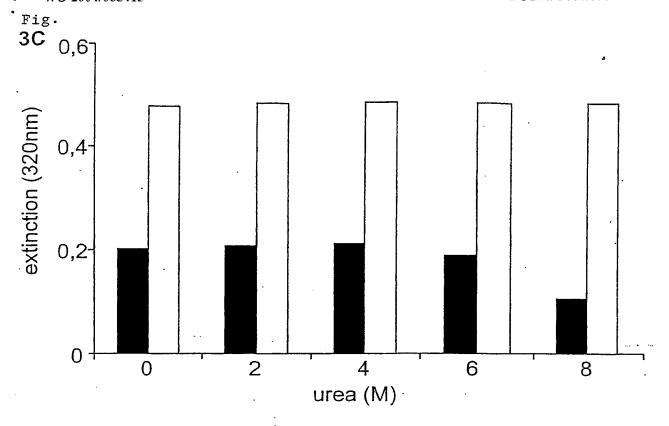












WO 2004/065415

10/542769 CT/EP2004/000423

Fig.

N-terminal sequence:

Internal peptide seguences

	Sequence	
1	DSGLDIAVFEYSDR	
2	LFXYQLPNTPDVNLEI	
3	VISELGLTPK	
4	XGDVPYDLSPEEK	
5	VILAXPVYALN	
6.	ATQAYAAVRPIPASK	
7	VFMTFDQP	
8	SDALFFQMYD	
9	SEASGDYILIASYADGLK	
10	NQGEDIPGSDPQYNQVTEP(L)(K)	

X = not determinable underlined: primer sequence for RT-PCR



Fig. 4B

1	Oligo-dT DBuTag1	tcc taa cgt agg tct aga cct gtt gca ttt ttt ttt ttt ttt
2	V-Fey 3 DTS 5'	tc gtg ttc gar tac tci gay cg
3	DBuTag1 DTS 3'	ctg tag gtc tag acc tgt tgc a
4	ATF Race 3' 660	ccg tgt aga tct cac tgc cat a
5	Abriged Anchor Primer	ggc cac gcg tcg act agt acg ggi igg gii ggg iig
6	ATF Race 3' 436	ccg ttg agt tgt aga cct
7	AUAP-EcoRI	aatt ggc cac gcg tcg act agt ac
8	ATF 5' Sign Eco RI GEX/ET	aa ttc tcg tct gct gtg ctt ctc ct
9	ATF 3' Xhol	gac tta gag gaa gta gtc gtt ga

11.12. 18.76.9

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Fig.

4C

- M S S A V L L L A C A L V I S V H A <u>D G TV C</u>
 ATGTCGTCTGCTGTCTCCTGGCTTGTGCGTCATCTCTGTCCACGCCGACGGTATCTGC
 . . . TCGTCTGCTGTGCTTCTCCTGGCCTTGTGCGTCATCTCTGTCCACGCCGACGGTGTCTGC
- G P G G A N S A Y M L R D S G L D I A V F E GGGCCTGGGGGGAGCTACCTCGCCTACATGCTGAGGGACTCCGGCCTGGACATCGCTGTTTCGAGGGGCCTGGGGGACATCGCTGTGTTCGAGGGGCCTGGGGGACATCGCTGTGTTCGAGGGGCCTGGGGGACATCGCTGTGTTCGAGGGGCCTGGGGGACATCGCTGTGTTCGAG
- E I G G M R F I E G A M H R L W R <u>V I S E L</u> GAGATTGGCGGCATGAGGTTCATCGAAGGCCCATGCACAGGCTCTGGAGGGTCATTTCAGAACTC GAGATTGGCGGCATGAGGTTCATCGAGGGCGCCATGCACAGGCTCTCGAGGGTCATTTCAGAACTC GAGATTGGCGCGCATGAGGTTCATCGAGGGCGCCATGCACAGGCTCTGGAGGGTCATTTCAGAACTC
- G Q S L T K K Q V K S <u>G D V P Y D J, S P E E GGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAGGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAGGACAGAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAG</u>
- EG P L K R E V A L K L T V P D G R F L Y D L GAGCCGCTCAAACGTGAGGTTGCGCTTAAACTAACCGTGCCGGACGGCAGATTCCTCTATGACCTC GAACCGCTCAAACGTGAGGTTGCGCTTAAACTAACCGTGCCGGACGGCAGATTCCTCTATGACCTC GGACCGCTCAAACGTGAGGTTGCGCTTAAACTAACCGTGCCGGACGGCAGATTCCTCTATGACCTC
- S F D E A M D L V A S P E G K E F T R D T H TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCCTGAGGGCAAAGAGTTCACCCGAGACACGCAC TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCCTGAGGGCAAAGAGTTCACCCGAGACACGCAC TCGTTTGACGAAGCCATGGA \Box CTGGTTGCCTCCCCTGAGGGCAAAGAGTTCACCCGAGACACGCAC

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Fig.

4C (continued)

- · V F T G E V T L DG A S A V S L F D D H L G E GTCTTCACAGGAGAGGTCACCTGGGAGAGGTCTCCCTCTTCGACGACCACCTGGGAGAGGTCTCCCTCTCGACGACGACCACCTGGGAGAGGTCTCCCTCTCGACGACGACCACCTGGGAGAGGTTTCACCGGAGAGAGCTCACCTGGACGACGACCACCTGGGAGAG
- D Y Y G S E I Y T L K E G L S S V P Q G L L GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTTCCGTCCCACAAGGGCTCCTA GACTACTA \overline{G} GGCAGTGAGATCTACACCCT \overline{G} AAGGAAGGACTGTCTTCCGTCCC \overline{G} CAAGGGCTCCTA GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTTCCGTCCCACAAGGGCTCCTA
- Q AT F L D A A D S N E F Y P N S H L K A L R CAGGCTTTTCTGGACGCCGCAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGACAGGCTTTTCTGGACGCCGCAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGACAGCTTTTCTGGACGCCGCAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA

- R P I P A S K V F M TS F D Q P W W L E N E R CGCCCGATTCCTGCAAGTAAGGTGTTCATGTCCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGGCCCCGATTCCTGCAAGTAAGGTGTTCATGACCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGCCCCCGATTCCTGCAAGTAAAGTTCATGACCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG
- K S W V T K S D A L F S O M Y D W Q K S E A AAATCCTGGGTCACCAAGTCGGACGCGCTTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG AAATCCTGGGTCACCAAGTCGGACGCGCTTTTCAGTCAAATGTACGACTGGCAGAAGTCTGAGGCG AAATCCTGGGGTCACCAAGTCGGACGCGCTTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG
- S G D Y I L I A S Y A D G L K A Q Y L R E L TCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTGTCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTGTCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGCCTCAAAGCCCAGTACCTGCGGGAGCTG
- K N Q G E D I P G S D P G Y N Q V T E P I, K AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTTACCGAACCCTCAAGAAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTCACCGAACCCCTCAAGAAGAATCAGGGAGAGACCCCTCAAGAAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTCACCGAACCCCTCAAG

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Fig.

4C (continued)

F H F D D V I S T M R R P S L K D E V Y V TTCCATTTCGATGACGTCATCAGCACCATGCGTCGCCCGTCACTGAAAGATGAGGT \overline{A} TACGTGGTGTCCATTTCGATGACGTCATCAGCACCATGCGTCGCCCGTCACTGAAAGATGAGGTCTACGTGGTGTTCCATTT \overline{A} GATGACGTCATCAGCACCATGCGTCGCCCCGTCACTGAAAGATGAGGTCTACGTGGTG

G A D Y S W G L I S S W I E G A L E T S E N GGAGCCGACTACTCCTGCTCTCCTGCATAGAGGGCGCTCTGGAGACCTCGGAAAACGGAGCCGATTACTCCTGGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCAGAAAACGGAGCCGATTACTCCTGGGGACCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC

V I N D Y F L GTCATCAACGACTACTTCCTCTAA
GTCATCAACGACTACTTCCTCTAA
GTCATCAACGACTACTTCCTCTAA

4D

W.J.

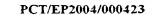
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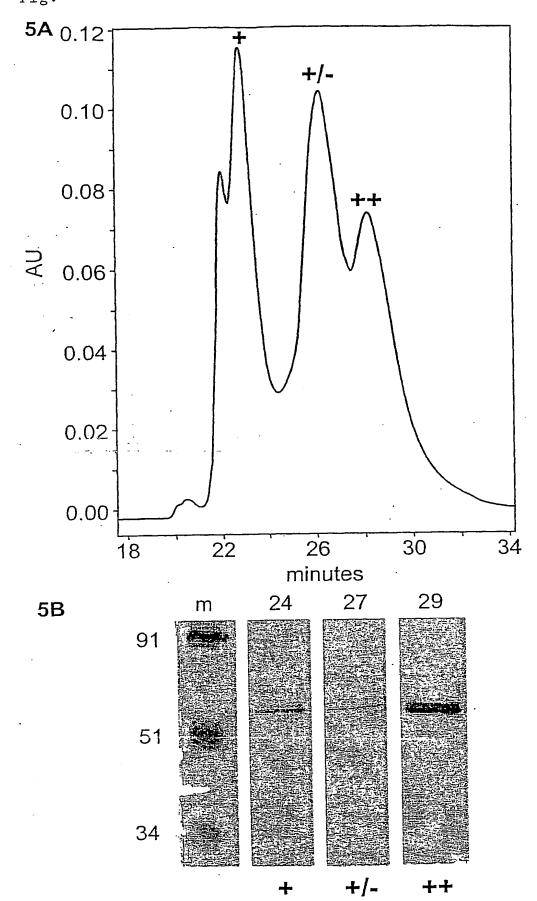
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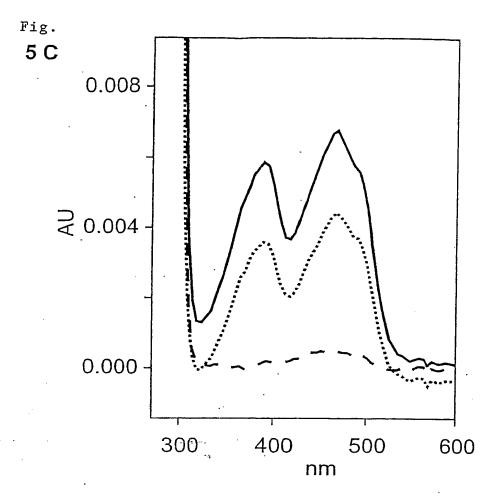
T Q H S

GPGGANSAYMLRDSGLDIAVFEYSDRVGGRLFTYQLPNTPDVNL

50 60 70 80



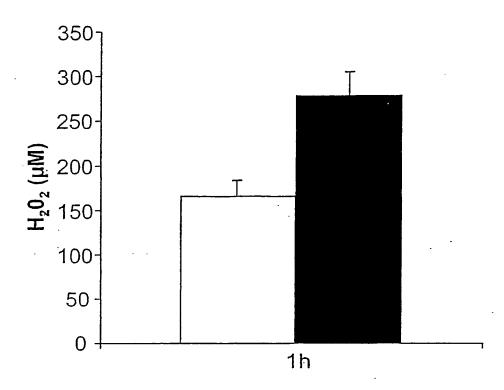


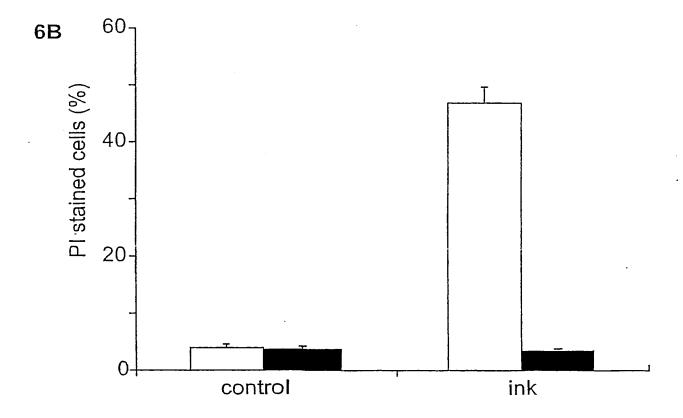


1.0000 1400 pm Fig.

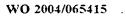
6**A**

Nii:

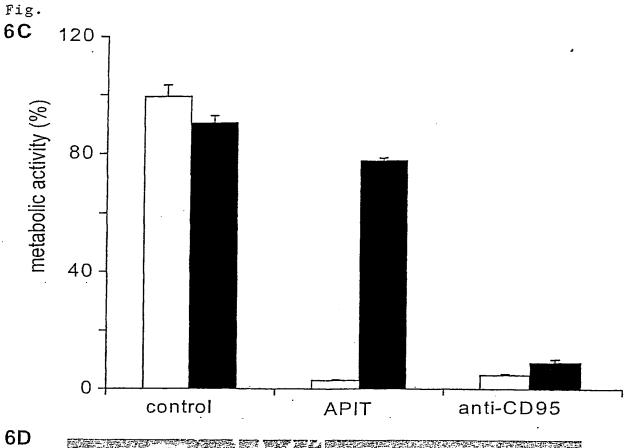




.



4.3



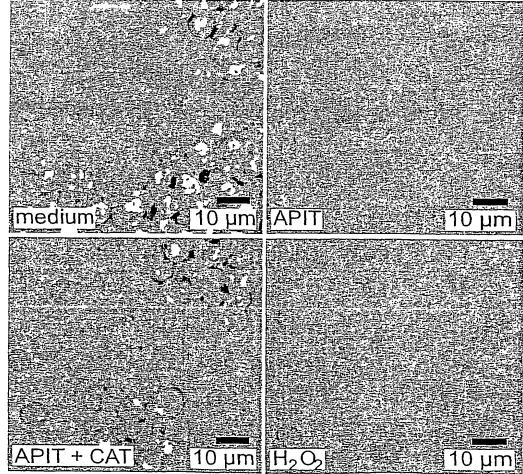


Fig. 6E

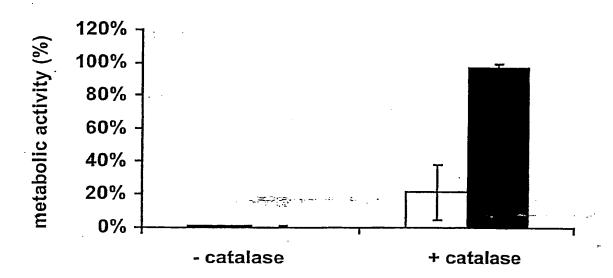
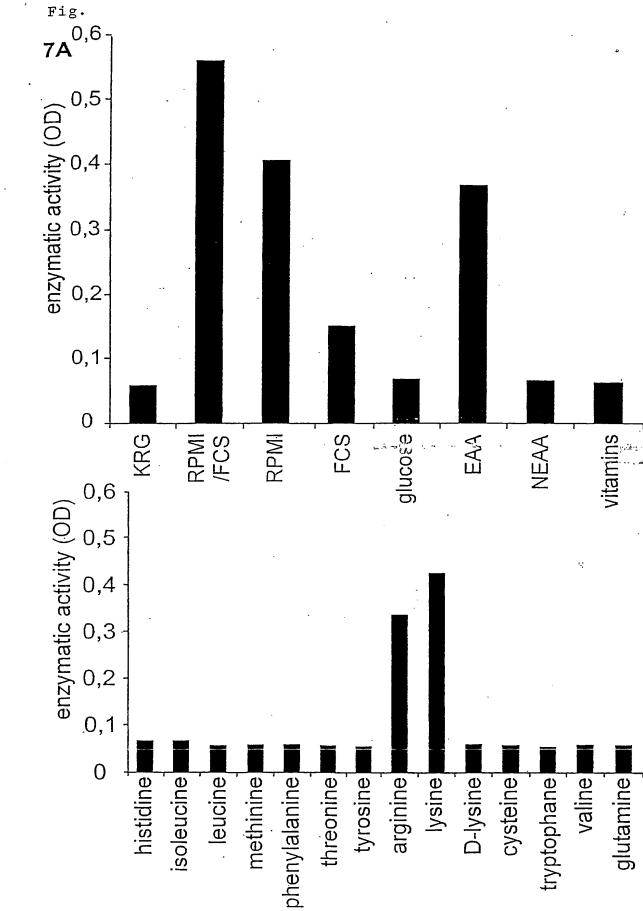
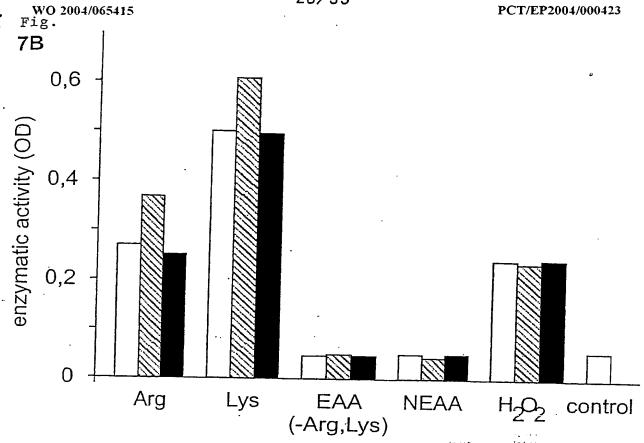
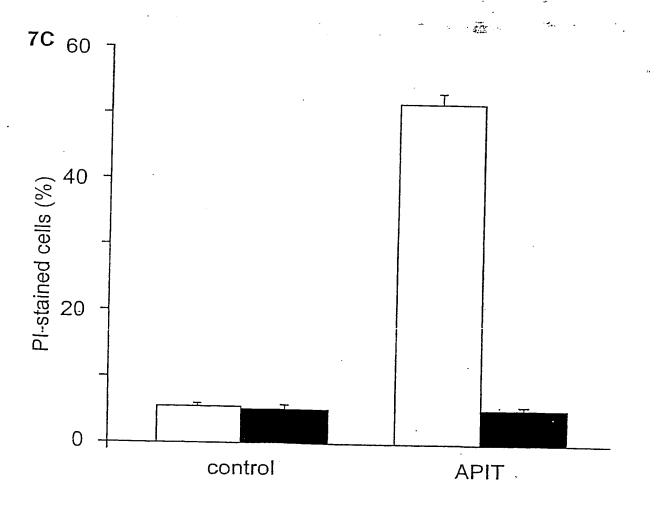


Fig.









time (min)

7D

metabolic activity (%)

7E

extinction (320nm)

R

NH

 α -imino acid

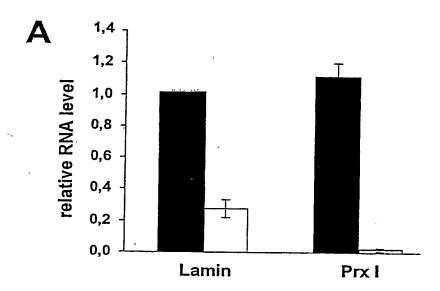
NH₄⊕

 α -keto acid

LAAO

L-amino acid

Fig. 8



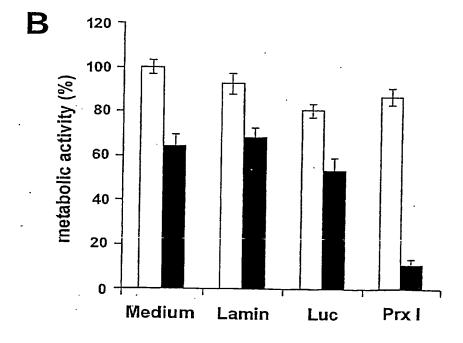
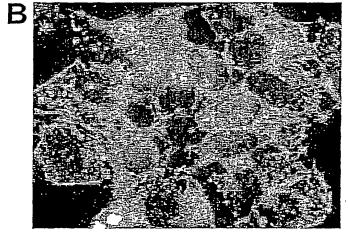


Fig. 9





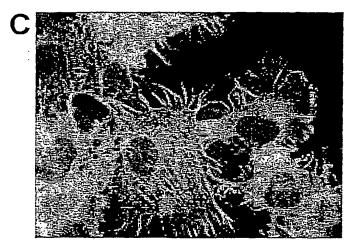
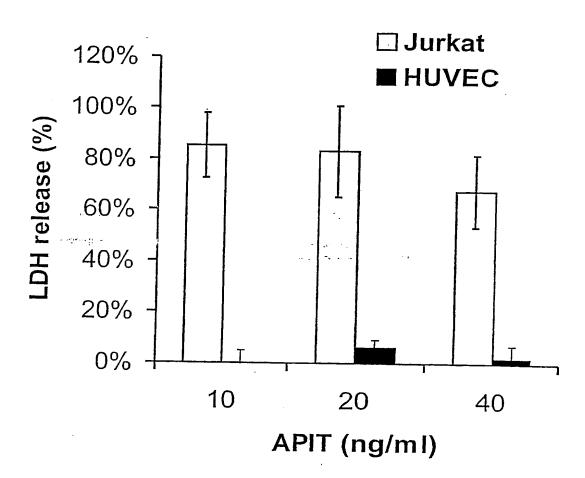


Fig. 10



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